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Sequence Listing was accepted.

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Reviewer: markspencer

Timestamp: [year=2010; month=1; day=12; hr=10; min=26; sec=44; ms=827; ]

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Application No: 10549506 Version No: 2.0

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**Finished:** 2009-12-21 18:59:42.409  
**Elapsed:** 0 hr(s) 0 min(s) 7 sec(s) 128 ms  
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**No. of SeqIDs Defined:** 21  
**Actual SeqID Count:** 21

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## SEQUENCE LISTING

<110> Bayer HealthCare LLC  
Haaning, Jesper Mortensen  
Andersen, Kim Vilbour  
Ropke, Mads  
Glazer, Steven

<120> FVII or FVIIa Variants

<130> 0272wo310

<140> 10549506  
<141> 2006-07-07

<150> US 60/456,547  
<151> 2003-03-20

<150> US 60/479,708  
<151> 2003-06-19

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<170> PatentIn version 3.5

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Ala  
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aat gcc ttt ctg gaa gag ctc cgc cct ggc tcc ctg gaa cgc gaa tgc 165  
Asn Ala Phe Leu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys  
5 10 15

aaa gag gaa cag tgc agc ttt gag gaa gcc cgg gag att ttc aaa gac 213  
Lys Glu Glu Gln Cys Ser Phe Glu Ala Arg Glu Ile Phe Lys Asp  
20 25 30

gct gag cgg acc aaa ctg ttt tgg att agc tat agc gat ggc gat cag 261  
Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln  
35 40 45

tgc gcc tcc agc cct tgc cag aac ggg ggc tcc tgc aaa gac cag ctg 309  
Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu  
50 55 60 65

cag agc tat atc tgc ttc tgc ctg cct gcc ttt gag ggg cgc aat tgc Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys	70	75	80	357
gaa acc cat aag gat gac cag ctg att tgc gtc aac gaa aac ggg ggc Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly Gly	85	90	95	405
tgc gag cag tac tgc agc gat cac acg ggc acg aag cgg acg tgc cgc Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys Arg	100	105	110	453
tgc cac gaa ggc tat agc ctc ctg gct gac ggg gtg tcc tgc acg ccc Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro	115	120	125	501
acg gtg gaa tac cct tgc ggg aag att ccc att cta gaa aag cgg aac Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn	130	135	140	549
145				
gct agc aaa ccc cag ggc cggtt atc gtc ggc ggg aag gtc tgc cct aag Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys	150	155	160	597
165				
ggg gag tgc ccc tgg cag gtc ctg ctc ctg gtc aac ggg gcc cag ctg Gly Glu Cys Pro Trp Gln Val Leu Leu Val Asn Gly Ala Gln Leu	170	175		645
180				
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195				
tgc ttc gat aag att aag aat tgg cgg aac ctc atc gct gtg ctc ggc Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu Gly	200	205		741
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gaa cac gat ctg tcc gag cat gac ggg gac gaa cag tcc cgc cgg gtg Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg Val	215	220	225	789
230				
gct cag gtc atc att ccc tcc acc tat gtg cct ggc acg acc aat cac Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His	235	240		837
245				
gat atc gct ctg ctc cgc ctc cac cag ccc gtc gtg ctc acc gat cac Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His	250	255		885
260				
gtc gtg cct ctg tgc ctg cct gag cgg acc ttt agc gaa cgc acg ctg Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu	265	270		933
275				
gct ttc gtc cgc ttt agc ctc gtg tcc ggc tgg ggc cag ctg ctc gac Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu Asp	280	285		981

cgg ggc gct acc gct ctc gag ctg atg gtg ctc aac gtc ccc cgg ctg			1029
Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg Leu			
290	295	300	305
atg acc cag gag tgc ctg cag cag tcc cgc aaa gtg ggg gac tcc ccc			1077
Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser Pro			
310	315	320	
aat atc acg gag tat atg ttt tgc gct ggc tat agc gat ggc tcc aag			1125
Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser Lys			
325	330	335	
gat agc tgc aag ggg gac tcc ggc ggg ccc cat gcc acg cac tat cgc			1173
Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg			
340	345	350	
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Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala			
355	360	365	
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Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu			
370	375	380	385
tgg ctg cag aag ctc atg cgg agc gaa ccc cgg ccc ggg gtg ctc ctg			1317
Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu Leu			
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Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp			
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Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln			
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Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn

65

70

75

80

Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly  
85 90 95

Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys  
100 105 110

Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr  
115 120 125

Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg  
130 135 140

Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro  
145 150 155 160

Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln  
165 170 175

Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala  
180 185 190

His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu  
195 200 205

Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg  
210 215 220

Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn  
225 230 235 240

His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp  
245 250 255

His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr  
260 265 270

Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu  
275 280 285

Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg  
290 295 300

Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser  
305 310 315 320

Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser  
325 330 335

Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr  
340 345 350

Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys  
355 360 365

Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile  
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Leu Arg Ala Pro Phe Pro  
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gcgcggggcc aatgccttc tggaaagagct ccgcctggc tccctggAAC gcgaatgcaa 180

agaggaacac agcagctttg aggaagcccg ggagatTTTc aaagacgctg agcggaccaa 240

actgtttgg attagctata gcgtggcga tcagtgcGCC tccAGCCttt gccagaacgg 300

gggctcctgc aaagaccAGC tgcagAGCTA tatctgcttc tgcctgcctg ccttgaggg 360

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cgagcagtac tgcagcgatc acacgggcac gaagcggagc tgccgctGCC acgaaggcta 480

tagcctcctg gctgacgggg tgcctgcac gcccacggtg gaataccctt gcgggaagat 540

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ggacgaacag tcccggggg tggctcaggt catcattccc tccacctatg tgccctggcac 840  
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